

FIG. 2

Out = Pre-assembled axonemal proteins
In (radial spokes, dynein arms)
Synthesized on free polysomes

IFT particle
Heterotrimeric Kinesin II
Cytoplasmic Dynein 1b

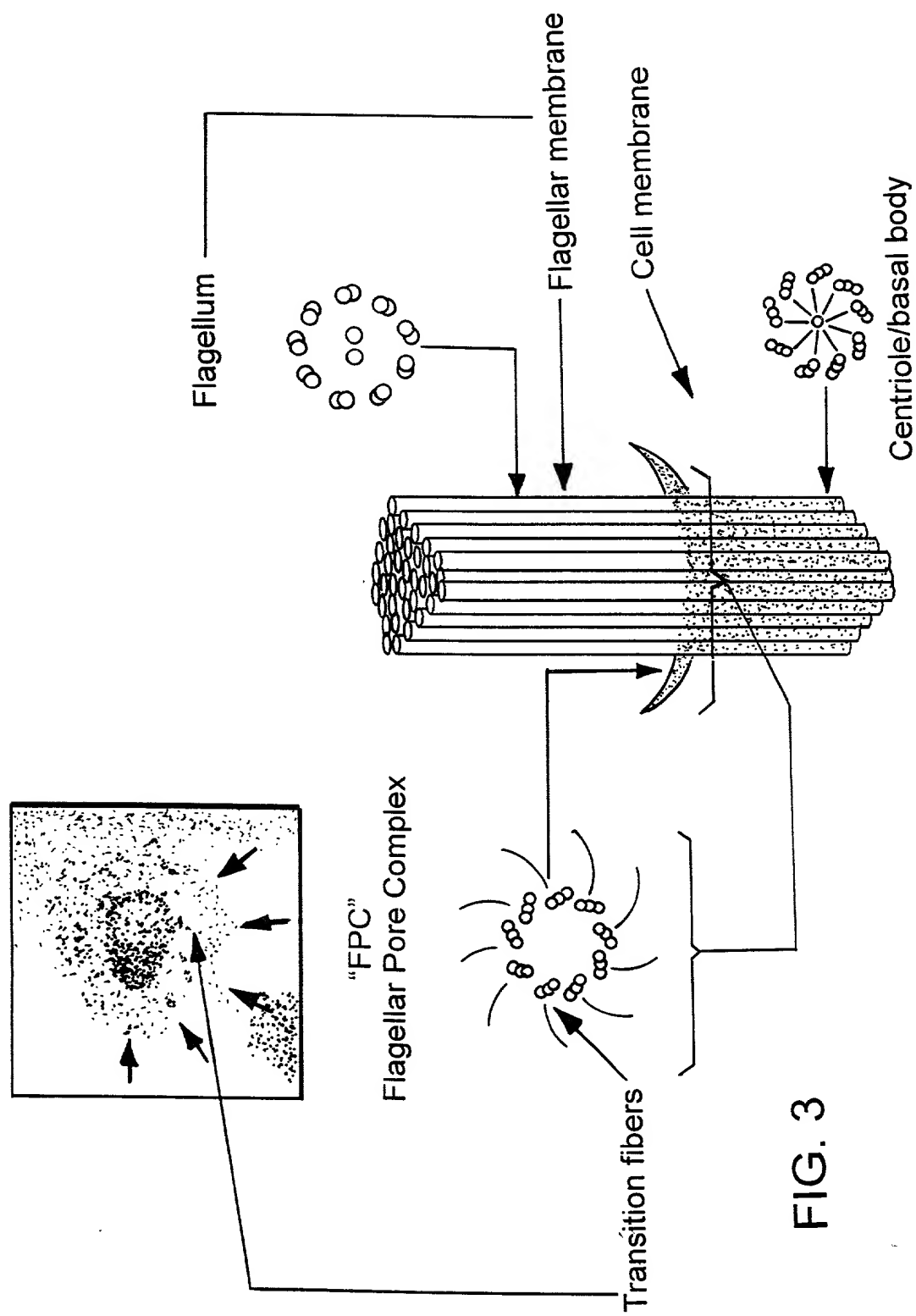


FIG. 3

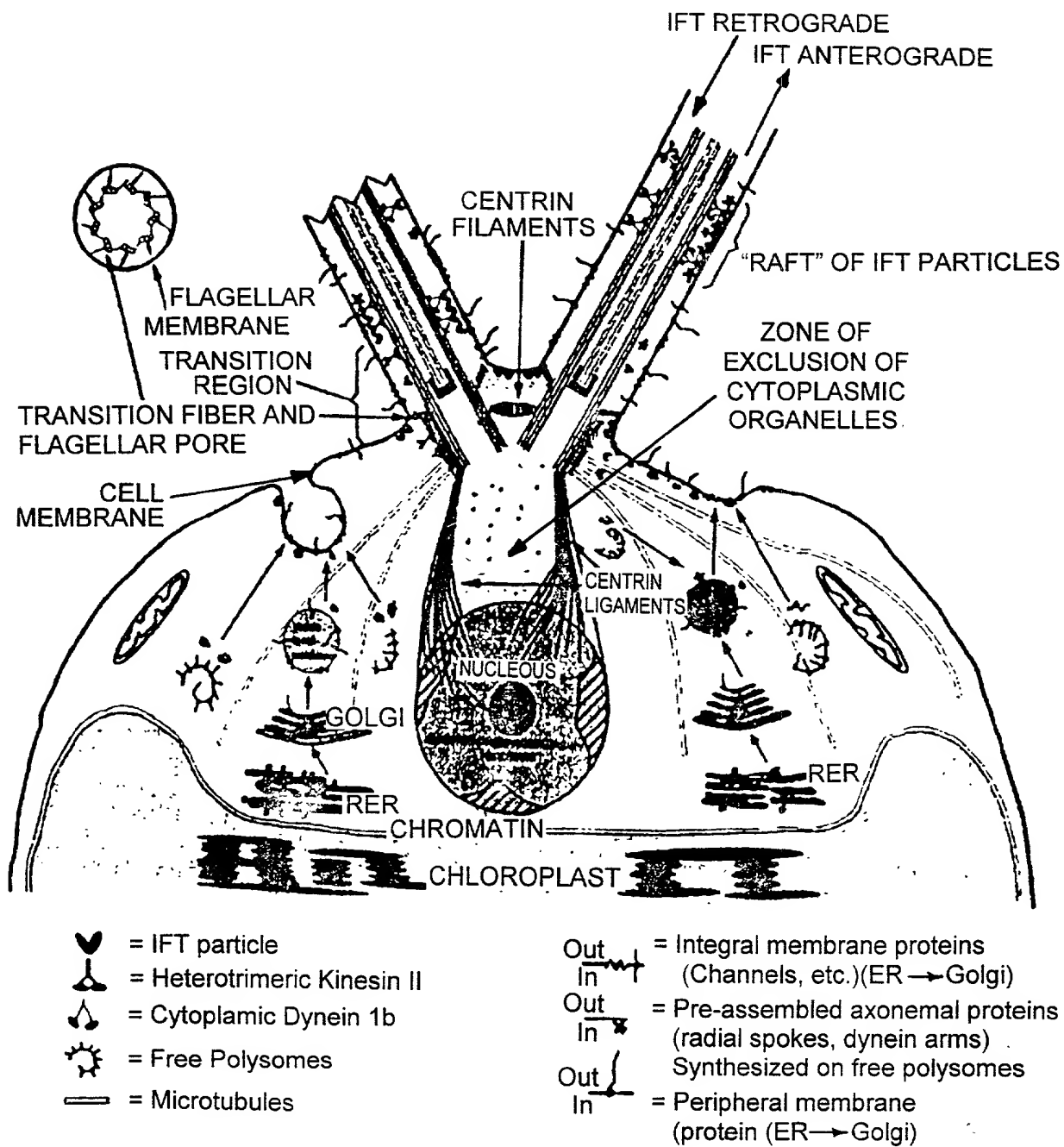
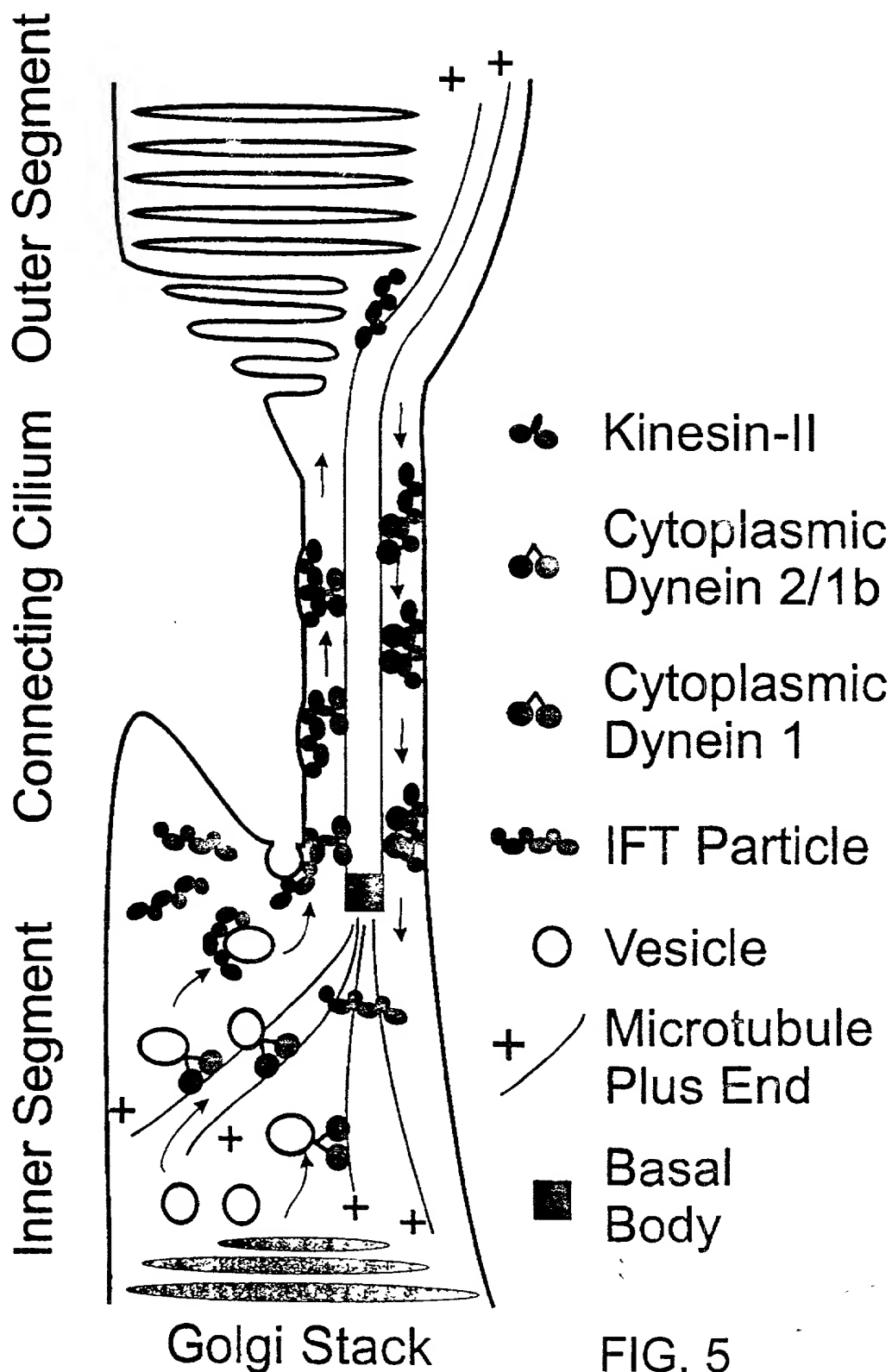


FIG. 4



IFT20

Chlamydomonas

>Cr_IFT20 predicted peptide

MDAVDRGVYFDEDFHVRILDVDKYNASKSLQDNTNVFINNIQNMQGLVDKYVSAIDQQVERLEA
EKLKAIGLRNRVAALSEERKRKQKEQERMLAEKQEELERLQMEEQSLIKVKGEQELMIQKLSOSS
SGAAYV (SEQ ID NO: 2)

FIG. 6A

>Cr_IFT20 cDNA

CACCGCTGCCGCTGAACAGAAAGTCTGCGCAGACTCGTCTTCTTGCCAAGTTCTTGCCAAAAC
CAGCAGGCCTAGAGGTTGCCTTAACCTAAATATACAAAACACAGAGCATCATGGACGCGGTA
GATAGAGGAGTCTACTTTGACGAGGACTTTCATGTCCGCATTCTTGATGTTGACAAGTACAAT
GCTTCAAAGTCGCTCCAGGACAACACAAATGTGTTTCATTAACAACATCCAAAATATGCAAGGC
CTCGTGGAACAAGTACGTGTCCGCCATCGACCAGCAGGTCGAGCGGCTAGAAGCTGAAAAGCT
GAAGGCCATTGGCCTGCGGAACCGGGTGGCTGCGCTGAGCGAGGAGCGGAAACGTAAACAA
AAGGAGCAGGAGCGCATGCTAGCGGAGAAGCAGGAGGAGCTTGAGAGGCTCCAAATGGAGG
AGCAGTCGCTGATCAAGGTGAAGGGCGAGCAGGAGCTCATGATTCAGAAGCTGTCCGACAGC
AGCAGCGGGGCGGCATACGTGTAAACGGTGTTCGGACGTCATGCGTGCAAAGGTAGTTTGCT
CTGTGAGGGTTGGCTGAGGCGGGCGAGGCTGCTATTGAGGCTGCAGCATGCGGTCTGGTGGC
AGATGTACATAACGGTATGGGGTGTGGCGACAGAACGAAACGGCGAGGGTGGCAGAAATGTC
GTGCAGAAGCGACGCTACAGCATCCATGGTACGTAGAGGCTTACTGGGTGTCAGTGCGTCGTC
CGCCACTGGGGACACACTTGCAGCGAGGAGCGCCATTGTTTGGCCACGGATTGCGTCAAGG
ACTTGAACGGCGCCAGTGAAGGCGGGGAATGGAATGTAAACAAACGACTCGAAAAAAAAAA
AAAAAAA (SEQ ID NO: 1)

FIG. 6B

Human

>Hs_IFT20-1 chr17 gb|AC002094.1|AC002094 [expressed]

MAKDILGEAGLHFDENLKLRLDPEVTQQTIELKEECKDFVDKIGQFQKIVGGGLIELVDQ
LAKEAENEKMKAIKARNLLKSIKQREAAQQQLQALIAEKKMQLERYRVEYEALCKVEAE
QNEFIDQFIFQK (SEQ ID NO: 23)

FIG. 6C

> Hs_IFT20-2 EST gb|AA584846.1|AA584846

QDSLGEAGLCFDELKVRDPEVT*QTRDPKEDCMDVFGKISPFQKEIVGGGLIEPVDQLAKAAENEK
RKVVGAWNLLQFMAKHREAQQQQLLAQTAEKMWLKRWWIEYE (SEQ ID NO: 24)

FIG. 6D

>Hs_IFT20-3 chr14 emb|AL121808.2|CNS01DSJ Human chromosome 14

MVKDILAEGLHFDENLKLWVLDSEVTQQTTELKEECKNFADKTGQFQKTVGGGLIELVDK
LAKKA*NAKMRAMVLR (SEQ ID NO: 25)

FIG. 6E

IFT27

Chlamydomonas

>Cr_IFT27 predicted peptide

MVKKEVKPIDITATLRCKVAVVGEATVGKSALISMFTSKGSKFLKDYAMTSG
VEVVVAPVTIPDTTVSVELFLDLAGSDLYKEQISQYWNGVYYAILVFDVSSMESFESCK
AWFELLKSARPDREPLRAVLVANKTDLPPQRHQVRLDMAQDWATTNTLDFFDVSANPPG
KDADAPFLSIATTFYRNYEDKVAAFQDACRNY (SEQ ID NO: 4)

FIG. 7A

>Cr_IFT27 cDNA sequence

ATGGTGAAGAAAGAAGTGAAGCCCATCGATATCACCGCAACGCTAAGATGCAAAGTAGCAGT
AGTCGGCGAAGCGACTGTCGGCAAGAGCGCGCTCATCTCTATGTTACGAGTAAAGGCAGCA
AGTTTCTAAAGGACTATGCGATGACGAGTGGGGTGGAGGTGGTGGTAGCCCCGGTGACCATT
CCGGACACGACGGTCTCGGTGGAGCTCTTTCTGCTGGACACGGCGGGGAGCGACCTGTACAA
GGAGCAGATATCGCAGTACTGGAACGGCGTATACTACGCCATTCTCGTGTTTCGATGTGAGCTC
TATGGAGTCCTTCGAGTCGTGCAAGGCGTGGTTTGAGCTGCTCAAATCGGCGCGTCCCGACCG
CGAGCGGCCCGCTGCGCGCCGTGCTGGTGGCGAACAAGACGGACCTCCGCGCGAGCGGCACC
AGGTGCGGCTGGACATGGCGCAGGACTGGGCCACCACCAACACCCTCGACTTCTTCGACGTGT
CCGCGAACCCGCCCCGGCAAGGACGCGGATGCGCCGTTCTGTCCATCGCCACCACCTTCTACC
GCAACTACGAGGACAAGGTGGCGGCCTTCCAGGACGCTTGCCGCAACTACTGA

(SEQ ID NO: 3)

FIG. 7B

Human

>Hs_IFT27 gi|12653581|gb|AAH00566.1|AAH00566 putative GTP-binding protein

MVKLAACILAGDPAVGKTALAQIFRSDGAHFQKSYLTGTGMDLVVKTVVPVDTGDSVELFIFDS
AGKELFSEMLDKLWESPNVLCVYDVTNEESFNNSKWLEKARSQAPGISLPGVLVGNKTDLAG
RRAVDSAEARAWALGQGLECFETSVKEMENFEAPFHCLAKQFHQLYREKVEVFRALA

(SEQ ID NO: 26)

FIG. 7C

IFT46

Chlamydomonas

>Cr_IFT46 predicted peptide sequence

MDDSMDYPDRDGDLDQFQGTARSQVVQNQPHDEEVNLSESESFAGADE
PPAAPRDASLIESHDMDEGPAAPARTLSPTGYEAGKHAPGGIANSDEAPPGAYNAQEYKH
LNVGEDVRELFYIGRYKPQTVELDTRIKPFIPDYIPAVGGIDEFIKVPRPDTKPDYLGL
KVLDEPAAKQSDPTVLTQLRQLSKEAPGAKADMVGRLEHTDENKAKKIQQWIASINDIH
KAKPAATVNYSKRMPEIEALMQEWPPEVETFLKTMHMPSGDVELDIKTYARLVCTLLDIP
VYDDPVESLHVLFTLYLEFKNNPIFRQHMENKLDGMSGGGGGMMGGGADVGL

FIG. 8A

(SEQ ID NO: 6)

>Cr_IFT46 cDNA sequence

ATGGATGACTCTATGGACTACCCTGACCGCGACGGGGACGACCTGGACCAGTTCAGGGCAC
CGCGCGCTCGCAGGTCTGTCAGAACAGCCGCACGACGAGGAGGTGAACCTGAGTGAGTCCG
AGAGCTTCGCGGGAGCGGATGAGCCTCCAGCTGCGCCTAGAGATGCGTCTCATAGAGTCA
CACGACATGGACGAGGGGCCAGCTGCTCCAGCGCGGACACTCTACCAACGGGCTATGAGGC
TGGAAGCACGCACCTGGCGGCATCGCCAACTCGGACGAGGCACCGCCGGGTGCTTACAACG
CACAGGAGTACAAGCACCTGAACGTGGGCGAGGACGTGCGCGAGCTGTTCTCCTACATCGGC
CGCTACAAGCCGCAGACGGTGGAGCTGGACACGCGCATCAAGCCCTTCATCCCTGACTACATC
CCCGCGGTGGGCGGCATCGACGAGTTCATCAAGGTGCCGCGACCCGACACCAAGCCCGACTA
CCTGGGGCTCAAGGTTCTGGACGAGCCGGCCGCAAGCAGTCGGACCCACGGTGCTGACGC
TGCAGCTGCGGCAGCTGTCCAAGGAGGCGCCGGGCGCCAAGGCCGACATGGTGGGGCGGCTG
GAGCACACCGACGAGAACAAGGCCAAGAAGATCCAGCAGTGGATCGCCTCCATCAACGACAT
CCACAAGGCCAAGCCGGCCGCCACCGTCAACTACAGCAAGCGCATGCCAGAGATCGAGGCGC
TGATGCAGGAGTGGCCGCGGAGGTGGAGACCTTCCTCAAGACCATGCACATGCCGTCCGGC
GATGTGGAGCTGGACATCAAGACCTACGCCCCGCTGGTGTGCACGCTGCTGGACATTCCCGTG
TACGACGACCCCGTGGAGAGCCTGCACGTGCTGTTCACACTGTACCTGGAGTTCAAGAACAAC
CCCATCTTCAGGCAGCACATGGAGATGGAGACAAGCTGGACGGCATGTCGGGCGGCGGCGG
CGGCATGATGGGCGGCGGCGCGGATGTGCTGGGCTTGTGA

(SEQ ID NO: 5)

FIG. 8B

Human

>Hs_IFT46 gi|8926685|emb|CAB96537.1| hypothetical protein [Homo sapiens]

MADNSSDECEEENKEKKKTSQLTPQRGFSENEDDDDDDSDSDDDDEEHGAPLEGAY
DPADYEHLPVSAEIKELFQYISRYTPQLIDLHKLKPFIPDFIPAVGDIDAFKLVPRPDGKPDNLGLL
VLDEPSTKQSDPTVLSLWLTENSKQHNTQHMVKVSLEDAEKNPKAIDTWIESISELHRSKPPATV
HYTRPMPDIDTLMQEWSPEFEELLGKVSLEDAEKNPKAIDTWIESISELHRSKPPATV
EFKNSQHFKALEGGKAFTPSNSTSQAGDMETLTF

(SEQ ID NO: 27)

FIG. 8C

[illegible][illegible][illegible][illegible][illegible][illegible]

[illegible][illegible][illegible][illegible]

Human

>Hs_IFT52 gi|4929575|gb|AAD34048.1|AF151811.1 CGI-53 protein [Homo sapiens]
MEKELRSTILFNAYKKEIFTTNNGYKSMQKKLRSNWKIQSLKDEITSEKLNQVGLWITAGPREKFT
AAEFEILKKYLDTGDDVLVMLGEGGESRFDTNINFLLEEYGIMVNNDVVRNVYHKYFHPKEAL
VSSGVLNREISRAAGKAVLAIIDEESSGNNALQALTFVYPFGATLSVMKPAVAVLSTGVCPLNRPI
LAFYHSKNQGGKLAVLGSCHMFSDQYLDKEENSKIMDVVVFQWLTTGDIHLNQIDAEDPEISDY
MMLPYTATLSKRNRECLQESDEIPRDFTTFLDLSIFQLDTSFHSVIEAHEQLNVKHEPLQLIQPQFE
TPLPTLQPAVFPPSFRELPPPPELFDLDETFSSEKARLAQITNKCTEEDLEFYVRKCGDILGVISKLP
KDQQDAKHILEHVFFQVVEFKKLNQEHIDTSETAFQNNF (SEQ ID NO: 28)

FIG. 9C

Caenorhabditis elegans

>Ce_Osm-6 gi|2292823|emb|CAA03975.1|osm-6 [Caenorhabditis elegans]
MPPFSDEKMTNRSIGRKVLIDQSKQQQISLISGFRGVARHLKSVLTVEINTEPINLNGLEDVRMLIIP
QPKTSFGTGEIEAIWKFVEEGGSLMILSGEGGERQSLNEMIAKYGITVNKDSVIRTVFLKYFDPKEA
LVANGVINRAIAVAACKNVSTEQKHNSQALSFIYPYGCTLDVNNRMSNVVLSSGSTSFPTSRPVAA
FHETKLNEMKKKGRVCVVGSVSMFHDTYIDKEENGKIFDTFVEFLVNGLELNTIDAAEPEINDYTN
IPDHIHMSQQIKVCMYEGELDQAISDFMKIMDTSLHSFNLKHWPM TIRLYEALNLSPPPLTLVEPQ
FELPMPPFQPAVFPPTFQELPMPPPELFDLDEQFSSPEIQLSQLANRSEEDLIFFIEKAGEITGISAEL
TRSERTPKKIIELAVSKLMLFKRSMMDGELEVASAFDIGEHDAHHQSFNQGEEMDEQLFSDIDEFD
DL (SEQ ID NO: 29)

FIG. 9D

IFT57

Chlamydomonas

>Cr_IFT57 predicted peptide sequence

MSSKRGRSSLAKAPEEAVNGEAFAPESP PPPGDDGDAGGEDGGAPPPPPATKGGPVAVGRS
LEIQTTDPVCMEMLADKLKLLNYEADFCRKKKPYRKPLSRLYFAVPLANSSEQFFYFTSLATWLL
GLAGVELPAPKEFDDPNLTCQNILGAVKKLGFAPPSYHPTKLTVGNGKEVVGVLDGLVDFVLERR
HHKYSRPAYGNDGQPEEGVQLDDEAEAAAMEGADELAMPAQNQADDDEEEEGVYVDPGRGDA
AGPGTGASAAMDAEKAVLVSKVDPTLWKIELERVAPKLRITIAADSKDWRSHLDEAHQHKEVISK
AWPDSKTSLERLRADLNGTLEKLQTREKFLNEQFESLMQQYRAARTTFTDVQETYNRKTEAVAD
RNQEMHRIGETLEEVKAMMDEKGSNIADATPVARIKTAIKQLNKELHDMEVRIQVVSHTLLQLSL
RNKRLLQAQAALSDEEED (SEQ ID NO: 10)

FIG. 10A

>Cr_IFT57 cDNA sequence

GTCTTGGGAACCCAGCGAGCCGCGCTCCTTGCCACATGTCCTGCTAGCTTCTGGTTTACACCGT
AGATTCATTTAAGCGAGAGACATGAGCAGCAAGCGGGGTGGGCGGTCATCCTTAGCAAAGGC
CCCCGAAGAGGCGGTAAATGGCGAGGCATTTGCGCCTGAGGCATCTCCCCCTCCACCCGGCG
ACGATGGAGATGCTGGTGGGGAGGACGGTGGCGCGCCTGCGCCCCCTCCGCCCCCGGCTACA
AAGGGCGGTCCAGTAGCTGTAGGAAGGTCGCTGGAGATACAAACAACGCCGGACGTGTGTCAT
GGAAATGCTGGCCGACAAGCTGAAGCTGCTAAACTACGAGGCGGATTTCTGCAGGAAGAAGA
AGCCCTACCGGAAACCCCTCTCGCGGCTCTATTTTTCGGGTGCCGCTCGCAAACCTCGAGCGAGC
AGTTCTTCTACTTTACCAGTCTGGCGACCTGGCTGCTGGGCTGGCTGGCGTGGAGCTGCCCCG
CTCCCAAGGAGTTTGATGACCCGAACCTTGACGTGCCAGAACATCCTGGGTGCGGTGAAGAAG
CTGGGCTTTGCGCCGCCAGCTACCAACCTACCAAGCTCACAGTGGGCAACGGCAAGGAGGT
GGTGGGTGTGCTGGATCGGGCTGGTGGACTTCGTGCTGGAGCGGCGGCACCAAGTACAGCC
GGCCCGCGTACGGAATGATGGGCAACCGGAGGAGGCGTGAACCTGGACGATGAGGCGGA
GGCTGCCGCGATGGAGGGTGGCGATGAGCTGGCGATGCCAGCCAGAACCGGCGATGACG
ATGAGGAGGAGGAGGGCGTATACGTGGACCCGGGGCGCGGTGACGCCGCGGGCCAGGGAC
AGGGGCATCCGCGGCGATGGACGCGGAGAAGGCGGTGCTTGTGTCCAAGGTGGACCCACGCG
TCTGGAAGATCGAGCTGGAGCGCGTGGCGCCGAAGCTGCGTATCACCATCGCCCGGACTCG
AAGGACTGGCGCTCACATCTGGATGAGGCGCACCAGCACAAGGAGGTGATCAGCAAGGCCTG
GCCCCAGACGAAGACGTCGCTGGAGCGCCTGCGTGCGGACCTGAACGGCACGCTGGAGAAGC
TGCAGACGCGTGAGAAGTTCTCAACGAGCAGTTTGAGAGCCTCATGCAGCAGTACCGCGCC
GCCCCGACCACGTTACGGACGTGCAGGAGACATAACAACCGCAAGACGGAGGCGGTGGCGGA
CCGGAACCGAGGATGCACCGCATCGGCGAGACGCTGGAGGAGGTGAAGGCCATGATGGAC
GAGAAGGGCAGCAACATCGCGGACGCCACGCCTGTGGCTCGCATCAAGACCGCCATCAAGCA
GCTTAACAAGGAGCTGCACGACATGGAGGTGCGCATCGGCGTGGTTAGCCACACGCTGCTGC
AGCTATCGCTGCGCAACAAGCGATTGCTGCAGGCGCAGGCGGCTCTCAGTGACGAGGAGGAG
GACTAGCTAGATCAGCGAGTGACAGAGGGCATGTGTGCGTACCGTGTGCGCGGGTACAGCCG
TGGGATGGAAGAGGTGATGTGGCGGGTTGCGGACCCAGCATTGCGTAGACCAGATCACTTAT
AGGTACAGAAAGACGGCTATATTGTTGGGGGCGGCGCACCCCTGGCTATGTATATACAAGCCG
TAGCGCAGAGCCGCTGCAAATGCGGTGCTGTGCCTGTGCTCCCGTGGGTGTGCGGCGTTCCGG
TCAAGTTTCATATAAGCTGTTGTGACTTGTGAGGCAGGCATGGCATATGGACAGGGCATCCCTG
CAAGGAAAGCAGGCAGCGGTATCCTTGTGGCGATGGGTCAAGCAGTGATGGAGGGCGCAAGC
GAGTTGCGGGCCTGTAAGCACAGGGTTGCCAAAAA (SEQ ID NO: 9)

FIG. 10B

Mouse

>Mm_IFT57 predicted peptide sequence

MAAAAIVIPPSGLDDGVSRARGEAGEAVVERGPGAAHYHMFVVMEDLVEKLKLLRYEEELLRK
SNLKPPSRHYFALPTNPGEQFYMFCTLAAWLINKTGRAFEQPOEYDDPNATISNILSELRSFGRTAD
FPPSKLKSGYGEQVCYVLDCLAEELKYIGFTWKRPSYPVEELEETVPEDDAELTLKVDDEEFVE
EETDNEENFIDLNVLKAQTYRLDTNESAKQEDILESTTDAAEWSLEVERVLPQLKVTIRTDNKDW
RIHVDQMHQHKSGIESALKETKGFLDKLHNEISRTLEKIGSREKYINNQLHLVQEYRGAQAQLSE
ARERYQQNGGVTERTRLLSEVTEELEKVKQEMEEKGSSMTDGTPLVKIKQSLTKLKQETVQMDI
RIGVVEHTLLQSKLKEKCNMTRDMHAAVTPESAIGFY (SEQ ID NO: 12)

FIG. 10C

>MmIFT57 cDNA sequence

GCGAAGGCTGCAGAGATCCTGGCCGGAGCCCAGCCGGGCGCTGGGGG
TCTGAGCAGGGATGGCCGCCGCGCGCGGTGATCCCGCCGTCGGGCTTGACGATGGGGTG
TCTCGGGCTCGCGGGGAAGGCGCAGGGGAGGCTGTGGTGGAGCGCGGGCCAGGAGCGGCCTA
CCACATGTTCTGTGGTGTGGAAGACTTAGTGGAGAAGCTGAAGCTGCTCCGCTACGAGGAGG
AGCTACTCCGAAAGAGCAATCTGAAGCCCCCGTCCAGACACTACTTTGCTCTGCCTACCAACC
CAGGCGAGCAGTTCTACATGTTTTGCACTCTTGCTGCGTGGCTGATCAACAAAAGTGGCCGTG
CCTTTGAGCAGCCTCAAGAATACGACGATCCCAATGCAACTATATCTAATATACTCTCTGAGC
TTCGCTCTTTTGGGAGAACTGCAGATTTTCTCCTTCAAATTAAGTCTGGTTACGGAGAACA
AGTGTGCTATGTTCTTGATTGCTTAGCTGAAGAAGCTTTAAATATATTGGTTTCACTTGGAAA
AGGCCATCATACCCAGTGGGAAGAACTAGAAGAAGAACTGTTCCAGAAGATGATGCCGAGTT
AACATTAAGTAAAGTGGATGAAGAATTTGTGGAAGAGGAGACAGATAATGAAGAAAAGTTTA
TTGATCTCAACGTTTTAAAGGCCAGACCTATCGCTTGGACACAAACGAGTCTGCCAAACAAG
AAGATATTTGGAATCTACGACAGATGCTGCGGAATGGAGCCTAGAAGTTGAGCGTGTACTAC
CGCAGCTGAAAGTCACGATTAGGACTGACAATAAGGATTGGAGGATCCATGTTGACCAAATG
CACCAGCACAAAAGTGGGATTGAATCTGCTCTGAAGGAGACCAAGGGGTTTTTGGACAAGCT
CCATAATGAAATTAGCAGGACTCTGGAAAAGATTGGCAGCCGAGAAAAGTACATTAACAATC
AACTTGAGCACTTGGTTCAAGAATATCGTGGGGCCCAAGCCAGCTAAGTGAGGCAAGGGAG
CGCTACCAGCAGGGCAATGGCGGAGTAACTGAACGGACCAGACTCCTCTCTGAGGTTACAGA
AGAATTAGAAAAGGTAAAGCAAGAAATGGAAGAGAAGGGCAGCAGCATGACGGACGGCACT
CCTTTGGTGAAGATTAAGCAGAGCTTAACCAAGCTGAAGCAAGAACTGTTTCAAGATGGACAT
TAGAATCGGTGTGGTGGAGCACACGCTACTTCAGTCAAACTCAAGGAGAAGTGCAACATGA
CCAGGGACATGCATGCAGCTGTACCCAGAGTCAGCAATTGGCTTCTATTAAACACGTGGGC
TTCCATGCTTCTGATTATTTCTGTTTTATATCAAATGATTTTTTAATGTTGCATTGATTTCCAAA
CACAATTTATACTTCTTCAAGCATATTTCAGTGGGTATTTTTGCACATGTGTTAATATCATGGTG
ATTATGATGGCCAAAGCCTGTACAATGAATATAGTATTTAATAAAGTACTTAAATTAATAAAAA
AAAAAAAAA (SEQ ID NO: 11)

FIG. 10D

Human

>Hs_IFT57-1 gi|7022022|dbj|BAA91466.1| unnamed protein product [Homo sapiens]
MTAALAVVTTSGLEDGVPRSRGEGTGEVVLERGPGAA YHMFVVMEDLVEKLKLLRYEEEFRLKS
NLKAPSRHYFALPTNPGEQFYMFCTLAAWLINKAGRPFEQPQEYDDPNATISNILSELSFGRTADF
PPSKLKSGYGEHVCYVLDCFAEEALKYIGFTWKRPIYPVEELEEESVAEDDAELTLNKVDEEFVEE
ETDNEENFIDLNVLKAQTYHLDMNETAKQEDILESTTDAAEWSLEVERVLPQLKVTIRTNDKDW
IHVDQMHQHRSGIESALKETKGFLDKLHNEITRTLEKISSREKYINNQLENLVQEYRAAQAQLSEA
KERYQQGNGGVTERTRLLSEVMEELEKVKQEMEEKGSSMTDGAPLVKIKQSLTKLKQETVEMDI
RIGIVEHTLLQSKLKEKSNMTRNMHATVIPEPATGFY (SEQ ID NO: 30)

FIG. 10E

>Hs_IFT57-2 chromosome 12 [ESTS BF089172]
DQRIHVDQMYQHKSGIESSLKESKRFFDKLHNE
ISKLEKISHCEKYINHQLHRVQEYPAAQTQLSDVRSQQGSGGVIERTRLLSEATED
TEHVKLEMECKCSSMTDGDLSVKIKQSLTKLKQETVQMDIRIGVVEHTLL (SEQ ID NO: 31)

FIG. 10F

Caenorhabditis elegans

>Ce_IFT57 gi|7504754|pir|T22994 hypothetical protein F59C6.9 - Caenorhabditis elegans
MLHHIKSLKSVLSRGQEGRFGEKRHSNTTFTGIATDFTA AKLKSGAGENVIFILNSLADASLVHVG
FQWQKMIPPKEEDED TAVDEQDEDDND DIVEEPMNFLDDDDDDNVIEIDLKAQGLATESKNPLQ
SVLQSNTDAITWKQEVERVAPQLKITLKQDAKDWRLHLEQMNSMHKNVEQKVGNGVPYLDNMS
KDI AKALERIASREKSLNSQLASMM SKFRATDTRAELREKYKAASVGVSSRTETLDRISDDIEQL
KQIEEQGAKSSDGAPLVKIKQAVSKLEELQTMNVQIGVFEQSILNTYLRDHFNFSA NLLNIM
(SEQ ID NO: 32)

FIG. 10G

IFT72

Chlamydomonas

>Cr_IFT72 partial predicted peptide sequence (lacking N-terminal end)

VYVIQQEFAALKDRNEQQRKRVDEVLTERRLNLESKAKQAESK
MSEIQASMDQRLNSMPPSQRNEYTTLVAEQQLQADSKRFEEVLDELKALQASEGELAR
NPFKQRLSLQLEQIRALTGKKYELTEERQSKRSPEELRADLMAKIKRDNTEVEQMTQQI
RELQDQIKKMEERVKSLGGATSGAVAAEEKANREKFEELLAKERHLNFMDFGSPSRKAAK
MQEKQQKEDGIVGVLEKMKVMQGIIGSNLPSQKKYKEMQDELEYKKMQLENTQTTOERLK
EELTMRRTLEKIDTLEDKIKLELTQLAERQEAMEKEMGEFGSVEDIQRKANAARERMGA
CAVCCLKRKDLLRSIVAERGLKFQAKRAQLQDHNLQVQLEKMEAKLKNLSAGVFEMDEFI
KAKESETNYRQLASNIAALVDDLNVHVKKAVV (SEQ ID NO: 14)

FIG. 11A

>Cr_IFT72 partial Cdna sequence (lacking 5' end)

GTGTACGTGATCCAGCAGGAGTTCGCGGCGCTCAAGGACCGCAACGAGCAGCAGCGCAAGCG
CGTGGACGAGGTGCTCACGGAGCGCCTCAACCTCGAGTCCAAGGCCAAGCAGGCCGAGTCCA
AGATGTCTGAGATCCAGGCGTCCATGGACCAGCGCCTCAACTCTATGCCGCCAGCCAGCGCA
ACGAATACACCACGCTCGTGGCCGAGCAGCAGCTGCAGGCCGACAGCAAGCGCTTTGAG
GAGGTGCTGGACGAGCTGGACAAGGCGCTGCAGGCCAGCGAGGGCGAGCTGGCGCGCAACC
CCTTCAAGCAGCGCAGCCTGCAGCTGCAGGAGCAGATCCGCGCGCTCACGGGGAAGAAGTAC
GAGCTGACGGAGGAGGAGCGGCAGAGCAAGCGCTCGCCGAGGAGCTGCGCGCCGACCTCAT
GGCCAAGATCAAGCGAGACAACACCGAGGTGGAGCAGATGACGCAGCAGATCCGCGAGCTTC
AGGACCAGATCAAGAAGATGGAGGAGCGCGTCAAGAGCCTGGGCGGCGCCACCAGCGGCGC
GGTGGCGGCGGAGGAAAAGGCCAACCGCGAGAAGTTTGAGGAGCTGTTGGCCAAGGAGCGC
CACCTAAACAACCTTTATGGACGGCTTCCCCAGCCGCAAGGCCGCAAGATGCAGGAGAAGCA
GCAGAAGGAGGACGGCATCGTGGGCGTGCTGGAGAAGATGGTGAAGATGCAGGGCATCATTG
GCTCCAACCTGCCAGCCAGAAGAAGTACAAGGAAATGCAGGACGAGCTCGAGTACAAGAA
GATGCAGCTGGAGAACACGCAGACCACGCAGGAGCGGCTCAAGGAGGAGCTGACCATGCGG
CGCACAGAGCTGGAGAAGATCGATACGCTGGAGGACAAGATCAAGCTGGAGCTGACGCAGCT
GGCGGAGCGGCAGGAGGCCATGGAGAAGGAGATGGGCGAGTTCGGCAGCGTCGAGGACATC
CAGCGCAAGGCCAACGCCGACGCGAGCGCATGGGGGCCTGCGCAGTGTGCTGTTGAAGCG
CAAGGACCTGCTGCGCTCCATCGTGGCGGAGCGCGGCCTCAAGTTCCAGGCCAAGCGCGCGC
AGCTGCAGGACCACAACCTCCAGGTGCAGCTGGAGAAGATGGAGGCCAAGCTGAAGAATCTG
AGCGCGGGCGTATTTCGAGATGGACGAGTTCATCAAGGCCAAGGAGAGCGAGACCAACTACCG
CCAGCTGGCCTCCAACATAGCGGCGTGTTAGCAGACCTCAACGTGCATGTCAAGAAGGCCG
TGGTGTAAGAAGGAGGCAGTGGTGTAAGGGGTCTCCGGAGGAGGGCGCGTGCCGTTGTTGGG
GTGTTGGGGGCGCGCGCGAGAAGTACGTGCGTGTGGCGTTGTGCCTTTCAGCAGGCTGCACG
TGAGTACGGTAGTCAAGGTGAAGGGCGGCCTGGGCACAGGAGGATGCTGACGCCGTGACGG
GTGACGATGACAGGCCATCGCGAGTTTGATCTCTGCTGTCGAGTCATTGACTTGGGTTCCTAG
ACAGGTGCGGGCTACAAGCCCGGAGGTTGATGGCTCACCTCGCAGTGCGCGGACAGCAGGTGT
GGCGCATGCGCATGTGCCTCAGGAGCGCGGTGCGGACCAGGGAAGATGCGATGGGAGTAGGC
TAGGCCTGTGTGAGGGCCCTTGCCGAAGCGCCACGGCCATTCCATGGCCTGGCCCCGAAGGCA
GCGCTCGTGGTTGGATACTGACCAGCGGCGTCAAGCGGCGTACGATGTCAGAAGTGGAGCTA
CCGCCCCCTGCACAAGGGGTGATGTACATACTGTTATTTAGGAGTCCGCTGCTTATAGCTACTG
GACTGCAGAAGAAGGAGGCTGCAAGGATCTGATGGAGGCGCTGGTGTGTATGGATGACGCTG
TAAGAGATGCACAAGAGAAAAA (SEQ ID NO: 13)

FIG. 11B

>Hs_IFT72.gij13376669.reflNP_079379.1: hypothetical protein FLJ22621
MEEVMNGYNMLKAQNDRETQSLDVIFTERQAKEKQIRSVEEEIEQEKQATDDIIKNMSLENQVKY
LEMKTTNEKLLQELDTLQQQLDSQNMKKESLEAEIAHSQVKQEAVLLHEKLYELESHRDQMAIED
K SIGSPMEEREKLLKQIKDDNQEIASMERQLTDTKEKINQFIEEIRQLDMDLEE HQGEMNQKYKEL
KKREEHMDTFIETFEETKNQELKRKAQIEANIVALLEHCSRNI NRIEQISSITNQELKMMQDDL NFK
STE VQKSQSTAQNLTSDIQLRLQLDLQKMELLESKMTEE QHSLKSKIKQMTTDL E IYNDLPALKSSG
EEKIKLLHQERMILSTHRNAFKKIMEKQNI EYEALKTQLQENETHSQLTNLERK WQHLEQNNFAM
KEFIATKSQESDYQPIKKNVTKQIAEY NKTIVDALHSTSGN (SEQ ID NO: 33)

1. H_2O (g)	
1.00	1.00
1.01	1.01
1.02	1.02
1.03	1.03
1.04	1.04
1.05	1.05
1.06	1.06
1.07	1.07
1.08	1.08
1.09	1.09
1.10	1.10
1.11	1.11
1.12	1.12
1.13	1.13
1.14	1.14
1.15	1.15
1.16	1.16
1.17	1.17
1.18	1.18
1.19	1.19
1.20	1.20
1.21	1.21
1.22	1.22
1.23	1.23
1.24	1.24
1.25	1.25
1.26	1.26
1.27	1.27
1.28	1.28
1.29	1.29
1.30	1.30
1.31	1.31
1.32	1.32
1.33	1.33
1.34	1.34
1.35	1.35
1.36	1.36
1.37	1.37
1.38	1.38
1.39	1.39
1.40	1.40
1.41	1.41
1.42	1.42
1.43	1.43
1.44	1.44
1.45	1.45
1.46	1.46
1.47	1.47
1.48	1.48
1.49	1.49
1.50	1.50
1.51	1.51
1.52	1.52
1.53	1.53
1.54	1.54
1.55	1.55
1.56	1.56
1.57	1.57
1.58	1.58
1.59	1.59
1.60	1.60
1.61	1.61
1.62	1.62
1.63	1.63
1.64	1.64
1.65	1.65
1.66	1.66
1.67	1.67
1.68	1.68
1.69	1.69
1.70	1.70
1.71	1.71
1.72	1.72
1.73	1.73
1.74	1.74
1.75	1.75
1.76	1.76
1.77	1.77
1.78	1.78
1.79	1.79
1.80	1.80
1.81	1.81
1.82	1.82
1.83	1.83
1.84	1.84
1.85	1.85
1.86	1.86
1.87	1.87
1.88	1.88
1.89	1.89
1.90	1.90
1.91	1.91
1.92	1.92
1.93	1.93
1.94	1.94
1.95	1.95
1.96	1.96
1.97	1.97
1.98	1.98
1.99	1.99
2.00	2.00
2.01	2.01
2.02	2.02
2.03	2.03
2.04	2.04
2.05	2.05
2.06	2.06
2.07	2.07
2.08	2.08
2.09	2.09
2.10	2.10
2.11	2.11
2.12	2.12
2.13	2.13
2.14	2.14
2.15	2.15
2.16	2.16
2.17	2.17
2.18	2.18
2.19	2.19
2.20	2.20
2.21	2.21
2.22	2.22
2.23	2.23
2.24	2.24
2.25	2.25
2.26	2.26
2.27	2.27
2.28	2.28
2.29	2.29
2.30	2.30
2.31	2.31
2.32	2.32
2.33	2.33
2.34	2.34
2.35	2.35
2.36	2.36
2.37	2.37
2.38	2.38
2.39	2.39
2.40	2.40
2.41	2.41
2.42	2.42
2.43	2.43
2.44	2.44
2.45	2.45
2.46	2.46
2.47	2.47
2.48	2.48
2.49	2.49
2.50	2.50
2.51	2.51
2.52	2.52
2.53	2.53
2.54	2.54
2.55	2.55
2.56	2.56
2.57	2.57
2.58	2.58
2.59	2.59
2.60	2.60
2.61	2.61
2.62	2.62
2.63	2.63
2.64	2.64
2.65	2.65
2.66	2.66
2.67	2.67
2.68	2.68
2.69	2.69
2.70	2.70
2.71	2.71
2.72	2.72
2.73	2.73
2.74	2.74
2.75	2.75

IFT88

Chlamydomonas

>Cr_IFT88 predicted peptide

MSYGGTEEDDL YGGYDEQSNPLAGSGGA AFKALGADGAPPGTAMMGPPGTAMKSFVPGTA
MRGGTAMQQDPSLARPMTSNRGAGFTSAPNKKFDPLNRSMSGSTLGSSGGGAMLVARKGDT
SPEEQARGMEKTVHELLEKSAADAAKNDNSALENAMEAKKNERKLCRFREQNNMADQIN
LELMYAVDFNLAHMYHMKNKYSEALNLYTAIVRNKNFPQSGWLRVNMGNIHFEQKKYPSA
IKMYRMALDQISATAKEVRFKIMRNIGLSFVRMGQYPDALQSFATVMDNVPDHQTGYNLV
MCNYALSDREGMKNAFIKLLKVSPSEMDDDDDDDDPMGDDDDMQVMTMDDGLKDEMRRNT
IITRLIVKAAQLISEKVDRANGFEGGFMWCCEQLRDAGYTKLANEVELAKATRFMGQKQF
DKAVGVFKDFEKKKEPRVKARAATNLAFLYFLEGETDQADKYSEMALKSDRYNARAYVNKG
CVLVERGDLEGARSLFNEAAGIDPYCVEAIYNLGLVSQRLNELPYALAAFKKLHNMVDPN
VEVIHQIATTYDMMGDFKNAVKWFELLTSLVSNDPGVLARLGAIHARFDDEAKALHYYQE
SHRVYPVNMDVISWLGAYHVKSEVYEKAMPFFDLASKIQPQEVKWALMVASCYRRTNLP
AALGKYKQIHTQHPDNVECLRYLVHLCSELGRRAEAAEYMTKLKKA EKA AVPEATTAAAP
AAAAAGSGMGGMGGLDDDIGSSAVSAQNRGKKMLVKEHMGGGGGKDNDDWGNEQLGDDLL
PM (SEQ ID NO: 16)

FIG. 12A

>Cr_IFT88 gi|11528334|gb|AF298884.1|AF298884 Chlamydomonas reinhardtii protein IFT88 (IFT88)
 CGGCAACTTGACACTTGAGCTACTCGAAGGCAGGGCEGTGTGCAGAGCTCCTTCCCCACTATC
 CTCCTTTTGGCTACCATACCTTATCTTGCTAACAGCCTATAGAAGATGAGCTACGGGGGCACGG
 AGGAGGATGACCTTTATGGAGGATATGATGAGCAATCGAACCCGCTTGCGGGCTCGGGTGGT
 GCCGCATTTAAGGCACTTGGGGCCGATGGAGCTCCTCCAGGCACCGCCATGATGGGGCCGCT
 GGCACGGCCATGAAGAGCTTCGTGCCAGGCACGGCTATGCGGGGCGGCACGGCCGATGCAGCA
 GGACCCAGCCTGGCGCGGCTATGACCTCGAACCAGGGGTGCTGGCTTCACGTGGCGCCTAA
 CAAGAAGTTTGACCCCTCAATCGCTCAATGGGGTTCGACACTGGGGCTCGTCGGGGGGTGGCGC
 AATGCTGGTGGCTCGCAAGGGTGACACCAGCCCGGAGGAGCAGGCGCGGGATGGAGAAG
 ACGGTGCATGAGCTGCTTGAGAAGAGCGCGGCGGACGCGGCTAAGAATGACATCAACTCGGC
 CCTGGAGAACGCCATGGAGGCGAAGAAGAATGAGCGAAAGCTGTGCCGCTTCGGGAACAG
 AACAACATGGCGGACCAGATCAACCTGGAGCTGATGTACGCCGTGGACTTCAACCTGGCACA
 CATGTACCACATGAACAAGAATACTACAGCGAGGCGCTGAACCTGTACACAGCCATCGTGCGCA
 ACAAGAACTTCCCGCAGTCGGGTTGGCTGCGCGTCAACATGGGCAACATCCACTTCGAGCAG
 AAGAAGTACCCCTCCGCCATCAAGATGTACCGCATGGCGTTGGACCAGATCAGCGCCACCGC
 CAAGGAGGTCCGCTTCAAGATCATGCGCAACATCGGGCTGTCTGTTCTGTGCGCATGGGCCAGTA
 CCCCAGCGCGCTGCAGTCCTTCGCCACGGTCATGGACAACGTGCCCCGACCACAGACCGGCTA
 CAACCTGGTTCATGTGCAACTACGCGCTGAGCGACCGCGAGGGCATGAAGAACGCCTTCATCA
 AGCTGCTCAAGGTGAGCCCATCCAGCGAGATGGATGACGATGACGACGACGACCCCATGGGC
 GATGACGACATGCAAGTGATGACCATGGATGACGGGCTGAAGGACGAGATGCGCAAGCGCA
 ACACCATCATACGCGCCTATTGTCAAGGCCGCGCAGCTCATCTCCGAGAAGGTGGATCGCG
 CCAACGGCTTTGAGGGCGGCTTCATGTGGTGCTGCGAGCAGCTGCGCGACGCGGGCTACACC
 AAGCTGGCCAACGAGGTGGAGCTGGCCAAGGCGACCCGTTTCATGGGGCAAAAGCAGTTTGA
 CAAAGCCGTGGGCGTGTTCAGGACTTTGAGAAGAAGGAGCCGCGCGTCAAGGCGCGCGCCG
 CCACCAACCTGGCGTTCCTGTACTTCTGGAGGGCGAGACCGACCAGGCCGACAAGTACAGC
 GAGATGGGCGTCAAGAGCGACCGCTACAACGCACGAGCCTACGTCAACAAGGGATGCGTGCT
 GGTGGAGCGCGCGGATCTGGAGGGAGCGCGAAGCCTGTTCAACGAGGCTGCCGGCATCGACC
 CCTACTGCGTGGAGGCCATCTACAACCTGGGCCTGGTGAGCCAGCGCCTGAACGAGCTGCCGT
 ACGCGCTGGCGGCGTTCAAGAAGCTGCACAACATGGTGCCCCGACAACGTGGAGGTTCATCCAC
 CAGATCGCCACCACGTACGACATGATGGGCGACTTCAAGAACGCGGTCAAGTGGTTTGAAGT
 GCTCACCTCGCTGGTCAGCAACGACCCCGGCGTGCTGGCGCGACTGGGAGCCATCCACGCCA
 GGTTTCGACGACGAGGCCAAGGCGCTGCACTACTACCAGGAGTCGCACCGCGTGTACCCGGTG
 AACATGGACGTCATCTCCTGGCTGGGCGCCTACCATGTCAAATCGGAGGTGTACGAGAAGGC
 CATGCCCTTCTTTGACCTGGCCTCCAAGATCCAGCCGCGAGGAGGTCAAGTGGGCGCTAATGGT
 GCGTCCTGCTACCGCGCACCAACACCTGCCCGCGCGCTGGGCAAGTACAAGCAAAATCC
 ACACGCAGCACCCCGACAACGTTGAGTGCTGCGCTACCTGGTGACCTGTGCTCCGAGCTGG
 GCCGCCGCGCGGAGGCCGCGGAGTACATGACCAAGCTCAAAAAGGCGGAGAAGGCGGCGGT
 GCCCGAGGCAACGACAGCGGCGGCGCCCGCGCGGCGCAGCTGGCAGTGGCATGGGTGGCA
 TGGGCGGCTGACGACGACATTGGCAGCAGCGCGGTGTGCGCGCAGAACCAGCGGCAAGAAG
 ATGCTGGTCAAAGAGCACATGGGTGGCGGCGGTGGCAAGGACAACGACGACTGGGGAACG
 AGCAGCTTGGGGACGACCTGCTGCCATGTAAACCGCAGTGCTGCCACAGGGCTTGGCGGGG
 GCGGGGCGTCAGCGCAGCCAGTGGGGCTACCGCCGCGGCGCTGGCGGAGGTGGCGGCGGCGCA
 GCTGGCGGAGCCATGCGCGCCAGGGCCAGGGGCTGTGGGGAGGTGATGGCGAGGGCGAGG
 ACGACGACCACCTAAAGCGCTGGGGCTGGGGGTGGGGTTGGTGGGCGGCCGACGCGGGGGC
 GCGCTGTCTGCCGGCACGGGGCGCGTGAAGGCCGATGTCAGCCGCGCCGCTCTACCCGGA
 GTTCGGGGCCGAGCCTGCGTTTGAAAGGTGCTGAGCTTTGGCTCGGCTGGGACGTCCAGCGC
 ACTGCCTGAGCTGGCGTAAAGCCATTACCGCTGATGCAGCCCGCCATTCTGTGTGTGCGTAT
 ATGTGTGTGAATGTATGTGTGTGCTAGGTAAGCAGGATGCGTGTGCGTTTGTGTTTTCGCG
 CTGCGCCACTTTTGGCTGCAGGGGTCCCCAGGTCAAGTGTGAAGCCCGGCGGCGGAAATG
 GTGTCATGGCAGTTGCGGCGCATGTCATGCGGAAGTGAGCGAAGTGCAATAGGCTCCTGCAGG
 GCATGGATGCGTAGGAACAGGGCTTGAATGATATCACTATGTGGCGTTGACGGGGCCACAAC
 TTACATGGGAGAGGCACGCCGAAAGGGTGTGTGAGGATCAGGAGCTTGGACTTGGCGTAGTG
 CTGTACATGGTGCCAGTCTACGTGCGGGCATAGACACATACAGGACCTGTGCTGCTGCGGAGT
 CCGCATCTGCAGGAAGTCGTGCCGGGTGTCACGAGTGCGGACGATGCGGATTGTGGAGGAGT
 ACAGATGGGGCCATCGGACATACTGGCACAGTGGCACCAACCGGCCCCCTGCGACGCGATGCTC
 GCACGACCCTGTAAAGGTGAGCCCCAAAAA (SEQ ID NO: 15)

FIG. 12B

Humans

>gi|5729800|ref|NP_006522.1| Tg737 protein; Probe hTg737 (polycystic kidney disease)
MMQNVHLAPETDEDDLYSGYNDYNPIYDIEELENDAAFQQAVRTSHGRRPPITAKISSTAVTRPIA
TGYGSKTSLASSIGRPMTGAIQDGVTRPMTAVRAAGFTKAALRGSAFDPLSQSRGPASPLEAKKK
DSPEEKIKQLEKEVNELVVEESCIANSCGDLKLALEKAKDAGRKERVLRQREQVTTPENINLDLTY
SVLSNLASQYSVNEMYAEALNTYQVIVKKNMFSNAGILKMNMGNILKQRNYSKAIKFYRMALD
QVPSVKNQMRIKIMQNIGVTFIQAGQYSDAINSIEHMSMAPNLKAGYNLTICYFAIGDREKMKK
AFQKLITVPLEIDEDKYISPDHPHTNLVTEAIKNDHLRQMERERKAMAEKYITTSAKLIAPVIETSF
AAGCDWCVEVVKASQYVELANDLEINKAVTYLRQKDYNAVEILKVLEKKDNRVKSAAATNLS
ALYYMGKDKFAQASSYADIAVNSDRYNPAALTNGNTVFANGDYKAAEFYKEALRNDSSCTEAL
YNIGLTYEKLNRLEALDCFLKLHAILRNSAEVLYQIANIYELMENPSQAIEWLMQVVSVIPTDPQ
VLSKLGELYDREGDKSQAFQYYYESYRYFPCNIEVIEWLGAYYIDTQFWEKAIQYFERASLIQPTQ
VKWQLMVASCFRSGNYQKALDITYKDTHRKFPENVECLRFLVRLCTDLGLKDAQEYARKLRL
EKMKEIREQRIKSGRDGSGGSRGKREGSASGDSGQNYSSASKGERLSARLRALPGTNEPYESSNK
EIDASYVDPLGPQIERPKTAAKKRIDEDDFADEELGDDLLPE (SEQ ID NO: 34)

FIG. 12C

Caenorhabditis elegans

>Ce_Osm-5 gi|12659061|gb|AAK01173.1|AF314195_1 OSM-5 [Caenorhabditis elegans]
MANSTFREDDDDFYGGFDSYDKAYDIQNITQNPQFQQAVARSSHGRRPTASQMGFRDASSSYGKP
PGTMMGNQSRMGGRRTAMANNNEPARPMTAVRGAGYTSFANKVQAAERPLSTENSGENGEEKCR
QMENKVMEMLRSLASEKKKFKEALDKAKEAGRERAVVKHREQQGLVEMMNLDLTFTVLF
NLAQQYEANDMTNEALNTYEIIVRNKMFPNSGRLKVNIGNIHFRKREFTKALKYYRMALDQVPSI
QKDTRIKILNNIGVTFVRMGSYDDAISTFDHCVEENPNFITALNLILVAFCIQDAEKMREAFVKMIDI
PGFPDDDDYMKEKDDDDVLLNQTLNSDMLKNWEKRNKSDAEKAIITAVKIIISPVIAPDYAIGYEW
LESLKQSVHAPLAIELEMTKAGELMKNGDIEGAIEVLKVFNSSQDSKTASAAANLMLRFLQGGR
RLVDAQQYADQALSIDRYNAHAQVNQGNIAYMNGDLDDKALNNYREALNNDASCVQALFNIGLT
AKAQGNLEQALEFFYKLHGILLNNVQVLVQLASIESLEDSAQAIELYSQANSLVPNDPAILSKLA
DLYDQEGDKSQAFQCHYDSYRYFPSNLETVEWLASYLETQFSEKSINYLEKAALMQPNVSKWQ
MMIASCLRRTGNYQRAFELYRQIHRKFPQDLCLKFLVRIAGDLGMTEYKEYKDKLEKAEKINQL
RLQRESRSSQGRHSANSTHSLPPSGLTGLGSGSGGSSGGGTRQYSAHVPLLLDSGTPFTVAQRDM
KAEDFSYDDPVAISSRPKTGTRKTTTDTNIDDFGDFDDSLLPD (SEQ ID NO: 35)

FIG. 12D

IFT122

Chlamydomonas

>Cr_IFT122 partial predicted peptide sequence (lacking N-terminal end)

HEGHFRRAPHFAYAKETLLKMDDTKGLITLYVEAEKWDDAFLLLHAHPECRQDVYLPYAKWLSN
QDRFDEARLAYQEGGFPSLATRILEQLCANAVVETRYADAAFYYYQLAMEALKSIKNPPSNMAPS
DRSALERFTELYDRAEVYYAYEVVHKS VHSPFRTHPTDLFNASRFLLMRLLPREVPLGVSVVN
VVYVLAKQAVEAGAFKLARFAYNKLQTLVLPAAWQAEVDLASVVIRSKPFSKDLEDLLPVCWRCS
TTNPLLNTQGDY CINC GAPFIRSFVTFEHL PVVEFELEPGVDDEEAGRLLGEDAGMEAARRERKAE
RQAKAAEVGGNMLRLDQNEIDRMDDAFAAQMMVPNTTIRVDRAMLRRLKTA EVMVRTWPNPV
IPKQYFRSHGPGGA AVLQDPADTSSSRMSSRWRRWSVARRPSAAPPCAARAWRRARTPRMRVPA
ATSWAGRWAARVGPLGAPARRACPCPSSRAGRWCERGRLSGAYRVRGWIPDVGGE

(SEQ ID NO: 18)

FIG. 13A

>Cr_IFT122 partial cDNA sequence (lacking 5' end)

GGCACGAGGGCCACTTCCGCCGCGCGCCGCACTTTGCGTACGCCAAGGAGACGCTGCTCAAA
ATGGACGACACCAAGGGCCTGATCAGCTGTACGTGGAGGCTGAGAAGTGGGATGACGCCTT
CCTGCTGCTGCACGCGCACCCGAGTGCCGCGCAGGACGTGTACCTGCCCTACGCCAAGTGGCT
CAGCAACGAGGACCGCTTCGATGAGGCGCGGCTGGCGTACCAGGAGGGCGGCTTTCCAGCC
TGGCCACCCGCATCCTGGAGCAGTTGTGCGCCAACGCGGTGGTAGAGACGCGGTACGCGGAC
GCCGCTTCTACTACTATCAGCTGGCCATGGAGGCGCTCAAGAGCATCAAGAACCCGCCCTCC
AACATGGCGCCCTCGGACCGCTCCGCGCTGGAGCGCTTACGGAGCTGTACGACCGCGCCGA
GGTGTACTACGCCTACGAAGTGGTGACAAGTCCGTGCACTCGCCCTTCCGCACCACGCACCC
CGACACGCTCTTCAACGCCTCGCGCTTCTGCTCATGCGCCTGCTGCCGCCGCGCGAGGTGCC
GCTGGGCGTCAGCGTGGTCAACGTGGTGTACGTGCTGGCCAAGCAGGCTGTGAGGCGGGCG
CCTTCAAGCTGGCGCGCTTCGCGTACAACAAGCTGCAGACGCTGGTGTGCTGCCGGCGGCCTGGC
AGGCGGAGGTGGACCTGGCATCCGTGGTTCATCCGCTCCAAGCCTTTCTCAGACAAGGAGGAC
CTGCTACCGGTGTGCTGGCGCTGCTCCACCACCAACCCGCTGCTCAACACGCAGGGCGACTAC
TGCATCAACTGCGGCGCGCCCTTCATCCGCTCCTTCGTACCTTCGAGCACCTGCCCGTGGTGG
AGTTTGAGCTGGAGCCGGCGGTGGACGACGAGGAGGCGGGCCGCTGCTGGGCGAGGACGCG
GGCATGGAGGCGGCGCGGCGGCGAGCGCAAGGCGGAGCGGCAGGCCAAGGCGGCGGAGGTGG
GCGGCAACATGCTGCGGCTGGACCAGAACGAGATCGACCGCATGGACGACGCCTTCGCGGCC
CAGATGATGGTGGCCAAACACCACCATCCGCGTGGACCGGCCATGCTGCGGCGGCTCAAGAC
GGCCGAGGTGATGGTGCGCACCTGGCCCAACCCCGTTCATCCCAAGCAGTACTTCCGCAGTCA
TGGACCAGGAGGTGCCGCTGTGCTGCAGGACCTGCGGACACTTCTTCGAGCAGGATGAGTTC
GAGATGGCGGCGCTGGAGCGTGGCACGGCGCCCTTACGCCGACCAACCGTGGCGGGCGAGGG
CCTGGCGCCGGGCGAGGACGCCGAGGATGAGGGTGCCGGCGGCAACAAGCTGGGCGGGCCG
TTGGGCAGCGCGCGTGGGCCCATTGGGGGCGCCAGCAAGGCGCGCATGTCCGTGCCCTTCCA
GCAGGGCCGGCCGCTGGTGTGAGCGGGGTGCGCTATCGGGCGCTTACCGGGTGGTGGTGG
ATTCCGGATGTAGGCGGGGAATAGGAGCTGCCGGTAGTGGCGTTGCAGCAGGCCTTCGTAC
GCAGCAGAGGGGGCACGAGGAGGACGTGAACGGGTGTCTTCATGCTGCTTGTGGTCTGACTT
GGTAGGACGGGCGTGGTGGCATCATTAGGCTGCCCTGCCGGTCCACCATAGGAGCTGCGAT
GGGCCTGAAGCAAGGCCCATGCACGGTGGCCGGGCACATGATGCATGACGGGACAGAGCAGG
GGACTTGCTGGAACCAAGTGTACATATGCCCGCGCAGAGACTGCGTGTCTCGAAGCGGGCACA
AATTGGGACATGTGCGCGTACAGACAAACGATGATGATGACAGGATGACAGTTGTTGTGCGG
CAGGGGGGCTCCCAAGCCCAGTTGAGGCCCAGGCAGGTTTGGTTGAATGGGGATGCACAGTG
GCAGTGCTAATGCGCTGGCGCTATGAGCGTCCATGGTGTGGCGGCCTCAAGTACAAGACACC
TTATAGTAGTTCAATCTGCCCCGCAAAAAAAAAAAAAAAAAAAAAA

(SEQ ID NO: 17)

FIG. 13B

Human

>gi|11360072|pir|T43484 hypothetical protein DKFZp434K016.1 - human (fragment)

TLLQPLKGHKDTVYCVAYAKDGKRFASGSADKSVIIWTSKLEGILKYTHNDAIQCVSYNPITHQLA
SCSSSDFGLWSPEQKSVSKHKSSSKIICCSWTNDGQYALGMFNIGIIRNKNGEEKVKIERPGGSLS
PIWSICWNPSSRWESFWMNRENEDAEDVIVNRYIQEIPSTLKSAVYSSQGSEAAAAEPEEEDDSPRD
DNLEERNLILAVADWGQKVSFYQLSGKQIGKDRAFNDFPCCISYFTKGEYILLGGSQKQVSLFTKD
GVRLGTVGEQNSWVWTCQAKPDSNYVVVGCQDGTISFYQLIFSTVHGLYKDRYAYRDSMTDVIV
QHLITEQKVRIKCKELVKKIAIYRNRLAIQLPEKILYELYSDELSDMHYRVKEKIIKKFECNLLVVC
ANHIIICQEKRLQCLSFSGVKEREWQMESLIRYIKVIGGPPGREGLLVGLKNGQILKIFVDNLFAIVL
LKQATAVRCLDMSASRKKLAVVDENDTCLVYDIDTKELLFQEPNANSVAWNTQCEDMLCFSGG
GYLNIKASTFPVHRQKLQGFVVGYNGSKIFCLHVFSISAVEVPQSAPMYQYLDRLKFKEAYQIACL
GVTDTDWRELAMEALEGLDFETAKKAFIRVQDLRYLELISSIEERKKRGETNNDLFLADVFSYQG
KFHEAAKLYKRSGHENLAEMYTDLCMFEYAKDFLGSGDPKETKMLITKQADWARNIKEPKAAV
EMYISAGEHVKAIEICGDHGWVDMIDIAARKLDKAEREPLLLCATYLLKLDSPGYAAETYLKMGD
LKSLVQLHVETQRWDEAFALGEKHPEFKDDIYMPYAQWLAENDRFEEAQAFHKAGRQREAVQ
VLEQLTNNAVAESRFNDAAYYYWMLSMQCLDIAQDPAQKDTMLGKFYHFQRLAELYHGYHAIH
RHTEDPFSVHRPETLFNISRFLHSLPKDTPSGISKVKILFTLAKQSKALGAYRLARHAYDKLRGLYI
PARFQKSIELGTLTIRAKPFHDSEELVPLCYRCSTNNPLNNGVNCINCRQPFIFSASSYDVLHLVE
FYLEEGITDEEAISLIDLEVLPRKRRDRLQLEIANNSSQILRLVETKDSIGDEDPFTAKLSFEQGGSEFV
PVVVSRLVLRSMRSDVLIKRWPPLRWQYFRSLLPDASITMCPSCFQMFHSEDYELLVLQHGCCP
YCRCKDDPGP (SEQ ID NO: 36)

FIG. 13C

Caenorhabditis elegans

>Ce_Daf10 Z82266 F23B2.4

MTMKKISRKLGFHGEQVCIYDLAFKPDGSELLLAADNKKVYLFDVNEGGQMOTLKGHKDLVYTV
AWSHNGELFASGGADKLVLWNEKHGTLRYSHTDVIQCMFMNPNQILLTCALNEFGLWSTAD
KNVIKQRSVVRCSCAWNTDGTIFAIGHGDTITLRKGTNATEEPSIIIQRDNEPIWGIAFSSNRTFA
SRDSQGNPMGIDEIMAVIDWNKTLFSYSLDGTIESKNLEFEPHCISYCLNGEYLLIGGSDKILKIYT
RKGVLGTVQMDHVIWVSVTVRPNSQTVAMGCVDTIACYNLVFSTVHCVDHARYANRKSMT
DVFVQNLEYRTSSNICCHDLVKKMSLYDTKLAVQLSDKIQIYKQTGGVSKNERRKQLKYTLQDTI
RKDLSFSLMVVTHGHLVVCNDEKLECYDFKGIKRSWNMKSIVRYLRVLGGPAHRETLVLGTTD
GGVYKVFIDNDYPILLDSRKTAKCIDINANRTVLASIEDTLVCKWSDIATGETLLQEPGCYSVFN
TVNENLFAFTTNMMLHVRTLAPGHTTRGVGYVLGFVKNRTFCLVQYNLIPLEVPYTIHLYQYIER
GDFKEALRIACLGVVKNWDWKYLANKALDALEFDVARKAYKVRDRKMLRMVWELKKMKSNG
EPDAILRATILAYTKKFREAAKIFKENGFNAMELFTDMRMFDDVQEVMTTASGETKKMLMRK
RASWARDANQPKIAAEMLISSGDLDDKAALLIINDWLELAIEISHKIDRSLETMKKLSAYFIRKHE
FGLASRIFQSINDMKSIIVDMHVNAGHWTDFAFAIADRHHPKYVEDVYLPYARFLAERDRFEEAQAF
HRAGKEQEAMHVLEQLTSNSVNNRFADAGCGLNPLLGGMSCIH CETPFIISFVSFDILPLIEFKIE
NDISFDEAKELIESEPPLSDDDYNNPLRGLKKGIKEIILNRESLSKLEQGHVIIQTFPPPLAPKFLFNVM
SITIAQCKGCNKVFDLDDFEMA CLRKGHCPCRTSYDRNEAFFVDEEDEDNTNIPSFGQFSRFS

(SEQ ID NO: 37)

FIG. 13D

IFT139

Chlamydomonas

>Cr_IFT139 partial predicted peptide sequence (lacking C-terminal end)

MADRVLALVHYAREGYFRHVQTVCNVLKKRPGDGVLTFWRAYGLLMEGNTADAMRDLSSIQ
GNSDLELAVAAAQLLGHESAKVPDHAHDLQAKLEIEERTASDQPCHLASFYLYTKSKERARGL
VERVLRNQPDMPAQQVLLGWIIISQQQDDEYDMLFDESELDDALSHFEQAVEHDHNDLQALLGK
AKIMELKKQLGPCLDVLTEINVRFGWFPALVEKTRMLMMLGDWEQVTETLQRVLAADQQNIM
AQAWNCMISLTREGNNKQAAQLQDLFSSMNRQEPKNAELFFRVARPFGRACSDPTLLGITYLM
ADRAAQLRPEMAAYVVEAAAQKLMMDETTNATERFTQALQLDELNLEANAGALEAQIMAGELE
EAAGQIMFLEDMFTNAAAAGGKRGRTGDMDDDPDMADPSLGTSSDNPTLLYLKGLLAWKQ
GMPSEGLGLLERSIAALFSAAADFHGPSLELYAALNPARITAMVRLLLQSIGGEPRAPTEAPSPLISK
VTRALDLLNKQAPALQESALLHARALYLNGNLDGALRKAGEILRMNPEESSAHLICSVYVAQDK
PELAVSALDQAVSSNFAIRETPLYHVQAKVLVANNKLDDAKRVLESAMNLPGVRTALTVQORA
RLGRKVVEPTLHERATVYLLLADVLARQSKIPDAPEAKKYIQDAIREFEGTSEEVRTVADCELA
ARGDVEGALKKLRRIPKESPHYVKARMAMADIYLRIRKDKAAIYCYMDLVDHTPDYDSYCM
GEAFMQIQEPEKAVRA (SEQ ID NO: 20)

FIG. 14A

>Cr_IFT139 partial Cdna sequence (lacking 3' end)

GGGTAGTCGTAACGTCTCAAGTATCGGACGCACTATTTGCAACTGCTTATTTTCGCATGGCTCC
CCCATCAATGAACTTGCTTCGTCCCTATGGCCTCCCATCGAGCGTGCAAGGTATCACCGTGTAT
ACACATGCTAAATATACTTCGTAAATTGGAGTTCACCGCGGAGGCCTGAACATTTGCCGAAC
CGCTCCTGAGGAAGCAGAACGAATAGCAGTGCATACAAATAGCCATGGCGGACAGGGTACTT
GCCCTGGTCCATTACTATGCTCGCGAGGGCTATTTTAGACATGTGCAGACGGTGTGCAACGAA
GTGCTCAAGAAGCGGCCGGGAGATGGCGTACTCACATTCTGGCGTGCCTATGGACTGCTCATG
GAGGGCAACACGGCGGACGCCATGCGTGACCTCTCCAGCATCCAGGGCAATTCTGACCTTGA
GCTGGCGGTTCGACGCCGCGCAACTACTGGGTACGAATCCGCCAAGGTGCCCGACCACGATG
CCATCATTGACCTCCAAGCCAAGCTGGAGATCGAGGAGCGCACCGCCAGCGACCAGCCCTGC
CTGCACCTGGCCTCCTTCTACCTGTATACCAAGTCCAAGGAGCGCGCCCGCGGTCTGGTGGAG
CGCGTGCTGCGCAACCAGCCCGACATGGTGCCGGCGCAGGTTCTTCTGGGCTGGATCATCATC
AGCCAGCAGCAGGACGACGAGTACGACATGCTGTTTGACGAGTCCGAGCTGGACGACGCCCT
CAGCCACTTCGAGCAGGCGGTGGAGCACGACCACAACGACCTGCAGGCGCTGCTGGGCAAG
CCAAGATCATGGAGCTGAAGAAGCAGCTGGGGCCCTGCCTGGACGTGCTGACGGAGATCAAC
GTGCGCTTCGGCTGGTTCGTGCCGGCGCTGGTGAAAAGACGCGCATGCTCATGATGCTGGGC
GACTGGGAGCAGGTGACGGAGACGCTGCAGCGGGTGCTTGCGGCGGACCAACAGAACATCAT
GGCGCAGGCCTGGAAGTGCATGATCTCCCTACTCGCGAGGGCAACAACAAGCAGGCGGCCA
AGCAGCTGCAGGACCTGTTTACGCTCAATGAACCGCCAGGAGCCCAAGAACGCCGAGCTCTTC
TTCCGCGTCGCCCGGCCCTTCGCGCCGCTGGCCTGCAGCGACCCACGCTGCTGGGCATCACC
TACCTCATGGCCGACCGCGCCGCGCAGCTCAGGCCGGAGATGGCGGCCTACGTGGTGGAGGC
AGCTGCTCAGAAGCTGATGATGGACGAGACCACCAACGCCACGGAGCGCTTCACGCAGGCGC
TACAGCTGGACGAGCTGAACCTGGAGGCCAACGCGGGCGCGCTGGAGGCGCAGATCATGGCG
GGCGAGCTGGAGGAGGCGGCGGGGAGATCATGTTCTGGAGGACATGTTACCAACGCCCGC
GGCGGCTGGCGGCGGCAAGCGCAAGGGCCGCGGCACCGGCGACATGGACGACGACCCCGAT
ATGGCCGACCCAGTCTGGGCACCTCCTCCGACAACCCACGCTGCTCTACCTCAAGGGTCTG
CTGGCCTGGAAGCAGGGCATGCCGTCCGAGGGCCTGGGTCTGCTGGAGCGCTCCATTGCCGCG
CTGTTCTCCGCCGCCGCCGACTTCCACGGCCCCAGCCTGGAGCTGTACGCGGCGCTCAACCCG
GCGCGCATACCCGCAATGGTGCGGCTGCTGTGCAGAGCATCGGCGGTGAGCCGCGCGCTCC
CACTGAGGCGCCGTCTCCGCTCATCAGCAAGGTACACCCGCGCGCTGGACCTGCTGAACAAGCA
GGCGCCGCGCTGCAGGAGAGCGCGCTGCTGCACGCGCGCGCTGTACCTGAACGGCAACC
TGGACGGCGCGCTGCGCAAGGCGGGCGAGATCCTGCGCATGAACCCCGAGGAGAGCTCCGCG
CACCTGCTCATCTGTTCCGTGTACGTGGCGCAGGACAAGCCCGAGCTGGCCGTCAGCGCGCTG
GACCAGGCCGTCAGCAGCAACTTCGCGATCCGCGAGACGCCTCTGTACCACGTGGTCCAGGCC
AAGGTGCTGGTGGCCAACAACAAGCTGGACGACGCCAAGCGCGTCCTGGAGTCCGCCATGAA
CCTGCCGGGCGTGCGCACAGCGCTACCGTGCAGCAGCGCGCGCGACTAGGGCGCAAGGTGG
TCGAGCCACGCTGCACGAGCGCGCCACCGTGTACCTGCTGCTGGCGGACGTGCTGGCGAGG
CAGTCCAAGATACCGGACGCACCAGAGGCCAAGAAGTACATCCAAGACGCCATCCGCGAGTT
CGAGGGCACCAGCGAGGAGGTGCGCGTCACGGTGGCGGACTGCGAGCTGGCCATTGCGCGCG
GCGACGTGGAGGGCGCGCTCAAGAAGCTGCGGCGCATCCCCAAGGAGTCTCCGCACTACGTG
AAGGCGCGCATGGCCATGGCCGACATCTACCTGCGCCACCGCAAGGACAAGGCCGCTACAT
CAAGTGCTACATGGACCTGGTGGACCACGCCCCGACTACGACAGCTACTGCATGCTGGGCG
AGGCGTTCATGCAGATCCAGGAGCCGGAGAAGGCAGTGCGCGCT (SEQ ID NO: 19)

FIG. 14B

Human

>Hs_IFT139-1 ref|NT_005498.3|Hs3_5655 Homo sapiens chromosome 3
SFIQAGIIYYSQEKYFHHVQAAAVGLEKFSNDPVLKFFKAYGVLKEDREAIQELEYSLKEIRKTVSG
TALYYAGLFLWLIGRHDKAKEYIDRMLKISRGFREAYVLRGWVDLTSDKPHTAKKAIEYLEQGIQ
DTKDVLGLMGKAMYFMMQQNYSEALEVVNQITVTSGSFLPALVLKMQFLARQDWEQTVEMG
HRRILEKDESNIDACQILTVHELAREGNMTTQATNHVRNLKALETREPENPSLHLKKIIVVSRLVC
GSHQVILGLVCSFIERTFMATPSYVHVATELG YLFILKNQVKEALLWYSEAMKLDKDGMAGLTGII
LCHILEGHLEEA EYRLEFLKEVQKSLGKSEVRAPWGYGLLQDDVLCCPPTPTFQCKVAWTFTLPLP
TKSAQADIGTETRSSLPQVLIFLQALLMSRKHKGEEETTALLKEAVELHFSSMQGIPLGSEYFEKLD
PYFLVCIKEYLLFCPKQPRLPQGI VSPLLKQVAVILNPVVKAAAPALIDPLYLMAQVRYYSGELEN
AQSI LQRCELD PASVDAHLLMCQIYLAQGNFGMCFHCLELGVSHNFQVVRDHPLYHLIKARALN
KAGDYPEAIKTLKMKVILPALKKEEGRKFLRPSVQPSQRASILLELVEALRLNGELHEATKVMQDT
INEFGGTPEENRITIANVDLVLSKGNVDVALNMLRNILPKQSCYMEAREKMANYILQTLRDRRLYI
RCYELCEHLPGPHTSLLLGDALMSILEVSRPHSLAKWPPSLSPVGEKRTQRHFPHQPEKALEV
YDEAYRQNPHDASLASRIGHAYVKAHQYTKAIEYYEAAQKINGQDFLCCDLGKLLKLLKKVNKA
EKVLKQALEHDIGVQDIPSMNDVKCLLLAKVYKSHKKEAVIETLNKVIDRWTQALALDLQSRI
LKRVPLEQPEMIPSQKQLAASICIQFAEHYLA EKEYDKAVQSYKDVFSYLPTDNKVLMA DLMFRK
QKHEAAINLYHQVLEKAPGDNFLVLHKLIDLLRRSGKLEDIPAFFELAKKVSSRVPLEPGFN YCRGI
YCWHIGQPNEALKFLNKARKDSTWGQSAIYH MVQICLNP DNEVVGGEAFENLIPRSNTCSYMEKK
ELEQQGVSTA EKLLREFYPHSDSSQTQLRLLQGLCRLATREKANMEAA LGSFIQIAQAEKDSVPAL
LALAQA YVFLKQIPKARMQLKRLAKTPWVLSEAEDLEKSWLLADIYCQSGKFDLAE LLLRRCVQ
YNKAQSCYKAYEYMGFIMEKEQSYKDAVTNYKLA WKYSHHANPAIGKATSQGARET WEGGGQ
EPHHDPR TQGLYPGCYENQRGSQVTRVPPSLLSMSPVGFKLAFNYLKDKKFVEAIEICNDVSQQP
WWGGPGVVVGNPA (SEQ ID NO: 38)

FIG. 14C

>Hs_IFT139-2 ref|NT_005239.3|Hs2_5396 Homo sapiens chromosome 2
INYYCQERYFHHVLLVASEGIKRYGSDPVFRFYHAYGTLMEGKTQEALREFEAIKNKQDVSLCSLL
ALIYAHKDREAILES DARVKEQRKGAGEKALYHAGLFLWHIGRHDKAKEYIDRM IKISDGSKQGH
VLKAWLDITRGKEPYTKKALKYFEEGLQDGN DTFALLGK VSWRQNYSGALETVNQIIVNFP SFLP
AFVKKMKLQLALQDWDQTVETAQRLSNKIIFFSFCGRS QLILQKIQTLLERAFSLNPQQSEFATELG
YQMILQGRVKEALKWYKTAM TLDTSVSALVGFIQCQLIEGQLQDADQQLEFLNEIQQSIGKSAV
LIYLHAVLAMKKNK RQEEVINLLNDVLDTHFSQLEGLPLGIQYFEKLNPD FLEIVMEYLSFCPMQ
VSNYGFL LGDIEAAFN NLQHCHLEHNPSYADAHLLLAQVYLSQEKVKLCSQSLELCLSYDFK VQVR
DYPLYHLIKAQSQKKMGEIADA IKTLMAMSLPGMKRIGASTKSKDRKTEVD TSHRLSIFLELIDV
HRLNGEHEATKVLQDAIHEFSGTSEEVRVTIANADLALA QGDIERALSILQNVTAEQPYFIEAREK
MADIY LKHRKDKMLYITCFAITYYEAALKTGQKNYLCYDLAELL LKLWYDKAEKVLQHALAH
EPGMKARELQARVLKRVQMEQPD AVPAQKHLAAEICA EIAKHSVAQRDY EKAIKFYREALVHCE
TDNKVDNYMTLSRLIDLLRRCGKLEDVPRFFSMAEK RNSRAKLEPGFQYCKGLYLWYTGE PNDA
LRHFNKARKDRDWGQNALYNMIEICLNP DNETVGGEVFENLDGDSNSTEKQESVQLAVRTAEKL
LKELKPQTVQGHVQLRIMENYCLMATKQKSNVEQALNTFT EIAASEKEHIPALLGMATAYMILKQ
TPRARNQLKRIAKMNWNAIDAEFEKSWLLADIYIQSAKYDMAEDLLKRCLRHNRSCCKAYEY
MGYIMEKEQAYTDAALNYEMAWKYSNRTNPAVG (SEQ ID NO: 39)

FIG. 14D

Caenorhabditis elegans

>gi|7511091|pir||T29012 hypothetical protein ZK328.7 - Caenorhabditis elegans

MKVAANELAISTIHFLPGHIEKAKASIMMKDWRGVMDCIMNADQPEGSNPYIEVLRTVHGICYAG
EVSMCLKRTLQLLLKSLDENEATNHVLYARITKLLVSISGRDEKILRHARDFLTRALKISRKPDYVAL
SMRIAFGLGGAKEVSTLSQELVALDCEDSYAVLSSVVSMLMISRVSDARAQFDILPSAHPKLLESPL
YYLIASVLAQSKDKSFENFRQHIEENLVEMLRNQLQSFPFGLDYLSLFSSDLLYSAVEQCDFDYPLV
PIKAPDDCMKLTAKTLQMIYDVAPGLAHCTLQLARNSYLCSENTNAAEKWIEKVLDKDDSLADAHI
LRAELILDRGGKITDADDALVTGLNFNFKLRETSLYHLIKSKTFKKRNENDEAIKTLKMALQIPRKE
PSKNLFQPKESADTHKISVQLELIDTLQHMKRIQEAETMTDALAEWAGQPEQDQLVIAQAQLYL
TKGHVERALGILKKIQPGQSNFHLSTRIKMAEIYLEKKDKRMFAACYRELLKVEATPGSYSLLGDA
FMKVQEPEDAINFYEQALKMQSKDVQLAEKIGEAYVMAHLYSKAVNFYESSMNIYKDKNMRLK
LANLLLKLRFKCEKVLRAFFERDPEPVGTETIQTYIQFLLLLAECEHMDNDVPEAMNDFEKAKS
LHSRIQDKTLTAALKKEGARICNLQAELLYRRREFSQAVDICKQALAYHETDLKANLLLSKIFKEE
NKWTLVLQPCQTVIQVDPHNDEANSILADFYIRSEAAHASTSYTLLNTNPQHWHALSRVVLEF
CRNGEQNAAEKHLDRAKEVNPRCVTESGYNVCRGRFEWYTGQNEALRYYSRTKDSAAGWREK
ALYYMIDICLNPDNEIHDENSVENPETTKIYLVSELWKKLVNSKNLPNITSIYSENFQSTDRFLLAQ
NFIRMHTTDKSAIQAAALDEFNRMAFNADRSQVTNVGAVFGVARGHVLLKQVQKAKTVLKMVNG
RVWNFDDSDYLEKCWLMLADIYINQNKNDQAVTFLDLVFKYNCNCLKAFELYGYMREKEQKYV
EAYKMYEKAFMATKERNPGFGYKLAFTYLKAKRLFACIETCQKVLDLNPQYPKIKKEIMDKAKA
LIRT

(SEQ ID NO: 40)

FIG. 14E

Che-2

Chlamydomonas

>Cr_Che-2 predicted peptide sequence

MRLKVKQSSANVHSELTAAGVGNVWNEFTCSDDQTIHKWNMLGEPEQKVSTLDAYFTDMHW
YPVSSKKTQAGGTDVFAVACTDGSVKILSRTGRVEKSIEGHKGACISLRWSYDGTALATAGEDGS
VKIWSRNGMLRSTLAQADSPVYSIVWAYDCDQLCYCTGSNNVIKSLSSNAKQNAWKAHDGVVL
KVDWSPINHLIITGGEDCKYKVWDSFGRLLFQSGLFDYPVTSVAWAPSGELFAVGGFNTLQLCDR
MGWAYSКИHLNDTGSIMTLSWTADSTQLAGGGGSGGVVFGQVVDLALEDGKMQVTVVDDMRIV
VNDILNENADELPEFRDRVКVSLGYGYLIVATATQCHVYNTTNLGTPHIFDLKDTVLLLLQAERH
FLLLDNSAGIQIYTYEGRQICNPRFQGLRTELLNAQMITLSNDTIAVLDQQASGTTVRFFDTAQGRP
VGEPWQHTLEVKEIALSQAGTINDRQLIVIDNRNDLYLLPVMKRHVAKLAAMCDSARWHDSTAM
LSAMVDQRLCVWYYPSEVYVDKDLLAKTRYTKSDSDFGKSAQIQLFAGNRCLVRRSDGVLVSAA
TSPYPAVLYDMIRKQQWDKATRLCRFIKDPTMWATLAAMAMAAKELNTAEVAFAAIDEVDKTH
FVRKVKQIPTEEGRNAELAVYRRKPEEGESILLQAGLVFRAIKLNIKLFNWERALXLATQHKQHQD
TVLWYRQQFLKNAKLAESITRFMQMNESVVVDQAAVKKKIEEERIKESQRPQAKRYV

(SEQ ID NO: 22)

FIG. 15A

>Cr_Che-2 cDNA sequence

ATGCGTCTCAAGGTCAAGCAGTCCAGCGCGAATGTGCACAGCGAATTAACAGCAGCTGTGGG
CTGGAATGTCTGGAATGAACTGTTCACTTGTAGCGACGACCAGACTATTCACAAATGGAACAT
GCTGGGGGAGCCAGAGCAGAAGGTCAGCACTCTGGACGCATACTTCACGGATATGCACTGGT
ACCCCGTGAGCTCGAAGAAGACGCAAGCAGGCGGGACGGACGTATTCGCGGTGGCGTGACACA
GACGGCTCTGTAAAAATCCTCAGCCGCACGGGCCGCGTGGAGAAAGTCCATTGAGGGGCACAA
GGGCGCGTGTCATCTCGCTGCGCTGGAGCTATGACGGGACGGCACTGGCGACGGCGGGCGAGG
ACGGGTCGGTAAAGATCTGGTCGCGCAACGGCATGCTGCGCTCCACGCTAGCGCAGGCGGAC
AGCCCCGTGTACTCGATTGTGTGGGCCCTACGACTGCGACCAGCTGTGCTACTGCACCGGCTCC
AACGTGGTCATCAAGTCGCTGTCTCCCAACGCCAAGCAGAACGCGTGGAAGGCGCACGACGG
CGTGGTGCTCAAGGTGGACTGGAGCCCCATCAACCACCTCATCATCAGGCGGCGAGGACT
GCAAGTACAAGGTGTGGGACAGCTTTGGGCGGCTGTTCCAGAGCGGGCTGTTTCGACTACC
CGGTCACGTCGGTGGCGTGGGCGCCAGCGGCGAGCTGTTTCGCGGTGGGCGGCTTCAACACG
CTGCAGCTGTGTGACCGCATGGGCTGGGCCTACTCCAAGATCCACCTCAACGACACGGGCGAGC
ATCATGACTCTGAGCTGGACGGCGGACAGCACGAGCTGGCGGGCGGCGGCGGCGAGCGGCGG
CGTGGTGTTTCGGCCAGGTGGTGGACCTGGCGCTGGAGGACGGCAAGATGCAGGTGACGGTGG
TGGACGACATGCGCATTGTGGTGAACGACATCTTGAACGAGAACGCGGACGAGCTGCCCCGAG
TTCCGTGACCGCGTCATCAAGGTGTCGCTAGGGTACGGCTACCTGATCGTGGCCACCGCGACG
CAGTGCCACGTGTACAACACCACCAACCTGGGCACGCCGCACATCTTTGACCTCAAAGACACG
GTCACCCTGCTGCTGCAGGCTGAGCGGCACTTCTGCTGCTGGACAACCTCGGCGGGCATCCAG
ATCTACACCTACGAGGGCCGCCAGATCTGCAACCCGCGCTTCCAGGGCCTGCGCACCGAGCTG
CTGAACGCGCAGATGATCACGCTGTCCAACGACACGATAGCGGTGCTGGACCAGCAGGCCAG
CGGCACCACCGTGCGCTTCTTCGACACGGCGCAGGGCCGGCCAGTGGGCGAGCCGTGGCAGC
ACACGTTGGAGGTGAAGGAGATCGCGCTGAGCCAGGCCGGCACCATCAACGACCGCCAGCTC
ATCGTCATCGACCGCAACCGCGACCTGTACCTGCTGCCCCGTCATGAAGCGCCACGTGGCCAAG
CTGGCGGCCATGTGCGACTCGGCGCGCTGGCACGACAGCACCGCCATGCTGTCCGCCATGGTG
GACCAGCGCTGTGTGTGTGTTACTACCCAGCGAGGTGTACGTGGACAAGGACCTGCTGGCC
AAGACGCGCTACACCAAGTCCGACTCGGACTTTGGCAAGTCGGCCCAGATCCAGCTCTTCGCC
GGCAACCGCTGCCTGGTGCGCCGCTCCGACGGCGTGCTGGTCTCCGCCGCCACCTCGCCCTAC
CCTGCCGTACTGTACGACATGATCCGCAAGCAGCAGTGGGACAAGGCCACGCGGCTGTGTGCG
CTTCATCAAGGACCCACCATGTGGGCCACGCTGGCGGCGATGGCCATGGCGGCTAAGGAGC
TGAACACGGCGGAGGTGGCGTTTCGCGGCGATTGACGAGGTGGACAAAACGCACTTTGTGCGC
AAGGTGAAGCAGATCCCCACGGAGGAGGGCCGCAACGCCGAGCTGGCGGTGTACCGGCGCA
AGCCCCGAGGAGGGCGAGTCCATACTGCTGCAGGCCGGCCTGGTCTTCCGCGCCATCAAGCTG
AACATCAAGCTGTTCAACTGGGAGCGCGCGCTGSACCTGGCCACGCAGCACAAGCAGCACCA
GGACACGGTGCTGTGGTACCGCCAGCAGTTCCTCAAGAACGCCAAGCTCGCCGAGTCCATCAC
GCGTTTCATGCAGATGAACGAGTCGGTGGTTGTGGACCAGGCGGCGGTGAAGAAGAAGATCG
AGGAGGAGCGCATCAAGGAGTCGCAGCGGCCAGGCGCCAAGCGCTACGTGTAA

(SEQ ID NO: 21)

FIG. 15B

Human

>Hs_Che-2 gi|7243129|dbj|BAA92612.1| KIAA1374 protein [Homo sapiens]
IELVSCVGVWTTAEELYSCSDDHQIVKWNLLTSETTQIVKLPDDIYPIDFWFPKSLGVKKQTQAESF
VLTSSDGKFHLISKLGKVEKSVEAHCGAVLAGRWNYEGTALVTVGEDGQIKIWSKTGMLRSTLA
QQGTPVYSVAWGPDSEKVLVYTAGKQLIKPLQPNKVLQWKAHDGILKVDWNSVNDLILSAGED
CKYKVVWDSYGRPLYNSQPHEHPITSVAWAPDGELFAVGSFHTLRLCDKTGWSYALEKPNTGSIFN
IAWSIDGTQIAGACGNHVVFAHVVEQHWWEWKNFQVTLTKRRAMQVRNVLNDAVDLLEFRDRV
IKASLNYAHLVVSTSLQCYVFSTKNWNTPIIFDLKEGTVSLILQAERHLLVDGSSIIYLYSYEGRFIS
SPKFPGMRTDILNAQTVSLNDTIAIRDKADEKIIFLFEASTGKPLGDGKFLSHKNEILEIALDQKGL
TNDKIAFIDKNRDLCSITSVKRFGKEEQIIKLGTVMVHTLAWNDTCNILCGLQDTRFIVWYYPNTVY
VDRDILPKTLYERDASEFSKNPHIVSFVGNQVTIRRADGSLVHISITPYPAILHEYVSSSKWEDAVRL
CRFVKEQTMWACLAAMAVANRDMTTAEIAYAAIGEIDKVQYINSIKNLPSKESKMAHILLFSGNI
QEAEIVLLQAGLVYQAIQININLYNWERALELAVKYKTHVDTVLAYRQKFLETFGKQETNKRYLH
YAEGQLIDWEKIKAKIEMEITKEREQSSSSQSSKSIKLP (SEQ ID NO: 41)

FIG. 15C

Caenorhabditis elegans

>Ce_Che-2 gi|4468141|emb|CAB38019.1| CHE-2 protein [Caenorhabditis elegans]
MKLKLSASRKTRHTEMVCGVGWIGTEAILSAAADHVFLLTNTATNESQQILNMPETFFPTSLHIFP
RSQTKGGQNDVFAVSTSDGKINILSRNGKVENMVDANGAALCARWNSDGTGLLSSGEDGFVK
MWSRSGMLRSVLAQFATAVYCVAWDSTSSNVLYCNADHCYIKSLKMQVAPIKWKAHDGILCCD
WNPTSDLIVTGGEDLKFKVWDGFGQILFNSSVHDYPITSISWNTDGTLFAVGSHNLRLCDKSGWS
HSLEKMNAGSVMALSWSPDGTQLAVGTAAGLVFHAHIIDKRLTYEEFEIVQTQKTVIEVRDVSSE
VSRETLETKERISKIAILYKYLIVVTSSHIYIYSSKNWNTPTMIEYNERTVNIIVQCEKIFLVSDGMTIT
IFTYEGRKLINLNPQGVMALLDERKIDLANDTLVVRDRADNKVLHFFDPTTGKAQGDGNLKHEH
DIVELTVNQCGPLNDRNVAFRDQIGAVHIAMVKTFGVSQRMVKIGSLVEQLVFNDVTNMLCGISE
GKIAVWPLPNVAFHNRNLLQKSLIQKNIGSVGKFPQLANFAGNTIVIRKSDGCLLPYGTLIT
MASQSKWDQAIRLCRSIGNDTMWATFAGLAVLHKNMIVMEIAYAALEDDEKVSLINEIKDKTDK
ETRQAMQVVLTGKLADADVLLERSGLSFRSLMLNIQMFKWKRALELGLKNKQWLEIVMGYREK
YLNCGQKETDPLFLKHMSEVEIDWVHIRELIAAEKAGNN (SEQ ID NO: 42)

FIG. 15D